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OM nucleic - nucleic search, using sw model
Run on: December 2, 2002, 00:22:39 ; Search time 76.7209 Seconds
(without alignments)
10713.895 Million cell updates/sec

Title: US-09-856-979-7
Perfect score: 365
Sequence: 1 tcagccagaccatgggggc.....tccatcaagccgtcgcatg 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	365	100.0	365	AAF86443	Deleted E1 promote
2	365	100.0	1695	AAF86442	Rice E1 promoter.
3	365	100.0	2275	AAF86440	Oligonucleotide #1
4	365	100.0	2407	AAQ27488	GEL promoter and 5
5	365	100.0	2407	AAQ53881	Sequence comprisin
6	365	100.0	5228	AAF86439	Plasmid pT5172del
7	365	100.0	5349	AAV23239	T-DNA of pTTS24.
8	365	100.0	6539	AAZ91097	E. coli plasmid pT
9	365	100.0	6548	AAI61394	Plasmid pT5172. C

C 10	365	100.0	6548	21	AAZ91096	E. coli plasmid pT
C 11	365	100.0	7492	22	AAF86441	Plasmid pT5346. U
C 12	363.4	99.6	6548	17	AAT39336	Plasmid pT5174 use
13	360.4	98.7	6667	22	AAD03878	NotI fragment of p
14	360	98.6	1687	22	AAD03888	E1 promoter from r
15	35.2	9.6	1831	12	AAQ10213	BamHI G-P-J fragme
16	35.2	9.6	1831	12	AAQ10211	BamHI G-P-J fragme
17	34.4	9.4	1543	23	AAS92206	DNA encoding novel
18	33	9.0	1302	24	AAI69430	Human TGR-6 DNA.
C 19	33	9.0	1305	22	AAS07945	Human cDNA encodin
C 20	33	9.0	1305	22	AAH73513	Human G protein-co
C 21	33	9.0	1305	24	ABK12958	DNA sequence of hu
C 22	33	9.0	1993	24	AAD37669	Human G-protein co
23	32.8	9.0	42000	21	AAA63349	Streptomyces globi
24	32.8	9.0	63164	21	AAA63348	Streptomyces globi
25	32.6	8.9	517	20	AAZ32196	Corn hexose carrie
C 26	31.8	8.7	1020	22	AAS05311	Mouse alpha-1,3 ga
C 27	31.8	8.7	47981	22	AAF30757	Micromonospora meg
28	31.8	8.7	201143	24	ABK83568	Human DNA differen
C 29	31.6	8.7	660	24	ABL34265	Human immune syste
C 30	31.6	8.7	918	23	AAS56147	Salmonella typhi D
C 31	31.6	8.7	3001	21	AAH51747	Chromosome 13q31-q
C 32	31.6	8.7	3001	21	AAH51748	Chromosome 13q31-q
C 33	31.2	8.5	4403765	22	AAI99683	Mycobacterium tube
C 34	30.8	8.4	450	21	AAC35795	Zea mays DNA fragm
C 35	30.8	8.4	648	24	ABQ16664	Oligonucleotide fo
36	30.8	8.4	648	24	ABQ16665	Oligonucleotide fo
37	30.8	8.4	1442	23	AAS82722	DNA encoding novel
38	30.8	8.4	2739	24	ABQ90374	M. capsulatus gene
39	30.8	8.4	2739	24	ABQ90380	M. capsulatus gene
40	30.8	8.4	2833	22	AAH21930	Mouse metallopepte
41	30.8	8.4	2833	24	ABK71487	Murine CLZ_26 comp
42	30.6	8.4	300	24	ABL74341	Corn tassal-derive
43	30.6	8.4	914	22	AAI85445	Human polynucleoti
C 44	30.6	8.4	915	24	ABQ46268	Oligonucleotide fo
45	30.6	8.4	915	24	ABQ46269	Oligonucleotide fo

ALIGNMENTS

RESULT 1
AAF86443
ID AAF86443 standard; DNA; 365 BP.
XX
AC AAF86443;
XX
DT 25-JUN-2001 (first entry)
DE Deleted E1 promoter.
XX
KW Male sterile plant; RNAase inhibitor; E1 promoter; ds.
OS Synthetic.
XX
PN WO200124616-A1.
XX
PD 12-APR-2001.
XX
PF 12-SEP-2000; 2000WO-JP06222.
XX
PR 30-SEP-1999; 99JP-0279307.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Hamada K, Nakakido F;
XX
DR WPI; 2001-266212/27.
XX
PT Method for producing male sterile rice and maize by inserting RNAase
gene and RNAase inhibitor genes with promoters into the plant genome -
XX
PS Claim 8; Page 25; 29pp; Japanese.

DR WPI; 2001-266212/27.
XX
PT Method for producing male sterile rice and maize by inserting RNase
PT gene and RNase inhibitor genes with promoters into the plant genome -
XX
PS Disclosure; Page 17-19; 29pp; Japanese.
XX
CC The present invention relates to a method for producing male sterile
CC plants. The method comprises inserting a promoter fragment upstream of an
CC RNase gene and a second promoter, upstream of an RNase inhibitor protein
CC gene and inserting it into the plant genome. The method is useful for
CC producing male sterile tobacco, lettuce and rapeseed plants, but
CC preferably rice and maize. The present sequence is an oligonucleotide
CC used in the method of the present invention.
XX
SQ Sequence 2275 BP; 604 A; 496 C; 496 G; 679 T; 0 other;

Query Match 100.0%; Score 365; DB 22; Length 2275;
Best Local Similarity 100.0%; Pred. No. 4.2e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTTGCCATACATTAACCAACGTAAGAAG 60
Db |
926 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTTGCCATACATTAACCAACGTAAGAAG 857
QY 61 TCCTACACTCAACCTAACTGTGAACGGTCCCTCTGGCCCAACGGTCAGAAATGCACCTA 120
Db |
866 TCCTACACTCAACCTAACTGTGAACGGTCCCTCTGGCCCAACGGTCAGAAATGCACCTA 807
QY 121 ATGGACGGGACAACACTTCTTTCACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACGCG 180
Db |
806 ATGGACGGGACAACACTTCTTTCACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACGCG 747
QY 181 TGAGGTGCTTTCGCCATGACCGTCTCTGGTGTGTGCAGTCACTTTCGCCACGCTTGCACCG 240
Db |
746 TGAGGTGCTTTCGCCATGACCGTCTCTGGTGTGTGCAGTCACTTTCGCCACGCTTGCACCG 687
QY 241 TGACTCACCTGCCACATTTGCCCGCCGCGTCCGCGGCGCTACAAAAGCCACACACGCGACG 300
Db |
686 TGACTCACCTGCCACATTTGCCCGCCGCGTCCGCGGCGCTACAAAAGCCACACACGCGACG 627
QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
Db |
626 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 567
QY 361 CGATG 365
Db |
566 CGATG 562

RESULT 4
AAQ27488
ID AAQ27488 standard; DNA; 2407 BP.
XX
AC AAQ27488;
XX
DT 10-FEB-1993 (first entry)
XX
DE GE1 promoter and 5' gene portion.
XX
KW Immature; spikelet; microsporocyte; meiosis; anther; probe; leaf;
KW expression cassette; root; stamen; fertile pollen; ss.
OS Oryza sativa.
FH key Location/Qualifiers
FT promoter 1..2263
FT /*tag= a
FT /label= PE1_promoter_region
FT TATA_signal 2181..2187
FT /*tag= b
FT misc_signal 2211
FT /*tag= c

FT CDS /label= Transcription_initiation_site
FT 2264..2407
FT /*tag= d
FT /label= El_gene_5'_region
XX
PN W09213956-A.
XX
PD 20-AUG-1992.
XX
PF 06-FEB-1992; 92WO-EP00274.
XX
PR 08-FEB-1991; 91EP-0400318.
PR 27-SEP-1991; 91EP-0402590.
PR 10-DEC-1991; 91EP-0403352.
XX
PA (PLBZ) PLANT GENETIC SYSTEMS NV.
XX
PI Komari T, Michiels F, Morioka S, Scheirlinck T;
XX
DR WPI; 1992-300042/36.
XX
PT Stamen-specific plant promoters - for producing male-sterile or
PT male-fertility-restored monocotyledons, e.g. rice
XX
PS Disclosure; Page 47-48; 58pp; English.
XX
CC The sequences given in AAQ27486-88 are the promoter regions of stamen-
CC specific rice genes. These genes were isolated by using male flower-
CC specific cDNA's as probes (see AAQ27481-5). The gene sequences isolated
CC can be used for producing transgenic male-sterile monocots. These
CC promoters can be used to form expression cassettes which can be
CC used to provide gene expression predominantly in the stamen cells
CC of a plant, and do not provide gene expression in the other parts of
CC the plant that are not involved in the production of fertile pollen.
XX
SQ Sequence 2407 BP; 662 A; 543 C; 507 G; 695 T; 0 other;

Query Match 100.0%; Score 365; DB 13; Length 2407;
Best Local Similarity 100.0%; Pred. No. 4.3e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTTGCCATACATTAACCAACGTAAGAAG 60
Db |
1902 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTTGCCATACATTAACCAACGTAAGAAG 1961
QY 61 TCCTACACTCAACCTAACTGTGAACGGTCCCTCTGGCCCAACGGTCAGAAATGCACCTA 120
Db |
1962 TCCTACACTCAACCTAACTGTGAACGGTCCCTCTGGCCCAACGGTCAGAAATGCACCTA 2021
QY 121 ATGGACGGGACAACACTTCTTTCACCGTGTCTACTGTCTAGCATCCTGTAGACGGTGGACGCG 180
Db |
2022 ATGGACGGGACAACACTTCTTTCACCGTGTCTACTGTCTAGCATCCTGTAGACGGTGGACGCG 2081
QY 181 TGAGGTGCTTTCGCCATGACCGTCTCTGGTGTGTGCAGTCACTTTCGCCACGCTTGCACCG 240
Db |
2082 TGAGGTGCTTTCGCCATGACCGTCTCTGGTGTGTGCAGTCACTTTCGCCACGCTTGCACCG 2141
QY 241 TGACTCACCTGCCACATTTGCCCGCCGCGTCCGCGGCGCTACAAAAGCCACACACGCGACG 300
Db |
2142 TGACTCACCTGCCACATTTGCCCGCCGCGTCCGCGGCGCTACAAAAGCCACACACGCGACG 2201
QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
Db |
2202 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2261
QY 361 CGATG 365
Db |
2262 CGATG 2266

RESULT 5
AAQ53881
JD AAQ53881 standard; DNA; 2407 BP.

XX AAQ53881;
AC
XX 27-JUN-1994 (first entry)
DT
XX
DE Sequence comprising anther specific promoter of PE1 of rice.
XX
KW Maintainer gene; sterile; sterility; homogenous population; hybrid;
KW seed; fertility restorer gene; pollen lethality gene; Oryza sativa;
KW ds.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT misc_feature 1..2263
FT /*tag= a
FT /label= PE1.
FT /note= "Sequence comprising anther specific
FT promoter PE1."
FT TATA_signal 2181..2187
FT /*tag= b
FT misc_feature 2211
FT /*tag= c
FT /note= "Transcription initiation site determined by
FT primer extension."
FT misc_feature 2264..2266
FT /*tag= d
FT /note= "ATG translation start site."
XX
PN WO9325695-A.
XX
XX 23-DEC-1993.
XX
XX 11-JUN-1993; 93WO-EP01489.
XX
XX 12-JUN-1992; 92US-0899072.
XX 03-NOV-1992; 92US-0970840.
XX
XX (PLB2) PLANT GENETIC SYSTEMS NV.
XX
XX Leemans J, Williams M;
XX WPI; 1994-007552/01.
XX
XX Maintainer gene for maintenance of male-sterile plants -
XX comprises fertility-restorer gene and pollen-lethality gene
XX
XX Disclosure; Page 65-66; 87pp; English.
XX
XX A maintainer gene of plants, pref. a foreign chimeric gene,
XX comprises (a) a fertility restorer gene which comprises a fertility
XX restorer DNA and (ii) a restorer promoter capable of
XX directing the expression of the fertility restorer DNA and (b) a
XX pollen lethality gene that is selectively expressed in microspores
XX and/or pollen of the plant to prevent the production of functional
XX pollen and which comprises (i) a pollen lethality DNA and (ii) a
XX pollen specific promoter capable of directing expression of the
XX pollen lethality DNA. Plants transformed with this DNA (maintainer
XX plants) can be used to maintain a homogenous population of male
XX sterile plants for the production of hybrid seed. The PE1
XX promoter is an anther specific, male sterility promoter and is used
XX in the construction of a plant transformation vector comprising a
XX maintainer gene as described which can be used to transform rice
XX and other plants.
XX
SQ Sequence 2407 BP; 662 A; 543 C; 507 G; 695 T; 0 other;

Query Match 100.0%; Score 365; DB 15; Length 2407;
Best Local Similarity 100.0%; Pred. NO. 4.3e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAATTTACTACTATTGGCCATACATTAACCACTAAAG 60
 , |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1902 TCAGCCAGACCAATGGGGCAAATTTACTACTATTGGCCATACATTAACCACTAAAG 1961
QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCTCTGTCTGGCCAAACGGTGAGAAATGCACCTA 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1962 TCCTACACTCAACCTAACTGTTGAACGGTCTCTGTCTGGCCAAACGGTGAGAAATGCACCTA 2021
QY 121 ATGGACGGGACACACTTCTTTCACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACCG 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2022 ATGGACGGGACACACTTCTTTCACCGTGTCTACTGTCTACATCCTGTAGACGGTGGACCG 2081
QY 181 TGAGGTGCTTTCCCATGACCGTCTCTTGGTTGTTGCAGTCACATTGCCGACCGTTCACCG 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2082 TGAGGTGCTTTCCCATGACCGTCTCTTGGTTGTTGCAGTCACATTGCCGACCGTTCACCG 2141
QY 241 TGACTCACCTGCCACATTTGCCCGCCCGCGTCCGCGCGCCCTACAAAAGCCACACACCGCAG 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2142 TGACTCACCTGCCACATTTGCCCGCCCGCGTCCGCGCGCCCTACAAAAGCCACACACCGCAG 2201
QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCGGTGCG 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2202 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCGGTGCG 2261
QY 361 CGATG 365
 |||||
Db 2262 CGATG 2266

RESULT 6
AAF86439/c
ID AAF86439 standard; DNA; 5228 BP.
XX
AC AAF86439;
XX
DT 25-JUN-2001 (first entry)
XX
DE Plasmid pTS172delta.
XX
KW Male sterile plant; RNAase inhibitor; plasmid pTS172delta; ds.
XX
OS Unidentified.
XX
PN WO200124616-A1.
XX
PD 12-APR-2001.
XX
XX 12-SEP-2000; 2000WO-JP06222.
XX
PR 30-SEP-1999; 99JP-0279307.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Hamada K, Nakakido F;
XX
DR WPI; 2001-266212/27.
XX
PT Method for producing male sterile rice and maize by inserting RNase
PT gene and RNase inhibitor genes with promoters into the plant genome -
XX
PS Disclosure; Page 14-17; 29pp; Japanese.
XX
CC The present invention relates to a method for producing male sterile
CC plants. The method comprises inserting a promoter fragment upstream of an
CC RNase gene and a second promoter, upstream of an RNase inhibitor protein
CC gene and inserting it into the plant genome. The method is useful for
CC producing male sterile tobacco, lettuce and rapeseed plants, but
CC preferably rice and maize. The present sequence is a vector used in
CC the method of the present invention.
XX
SQ Sequence 5228 BP; 1384 A; 1307 C; 1263 G; 1274 T; 0 other;

Query Match 100.0%; Score 365; DB 22; Length 5228;
Best Local Similarity 100.0%; Pred. NO. 6.1e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TCAGCCAGACCAATGGGGGCAAAATTACTACTATTGGCATACATTAAACCACGTAAAAG 60
Db 2986 TCAGCCAGACCAATGGGGGCAAAATTACTACTATTGGCATACATTAAACCACGTAAAAG 2927

QY 61 TCCTACTACTCAACCTAACTGTTGAACGGTCCTGTTCTGGCAACGGTGAGAATGCACCTA 120
Db 2926 TCCTACTACTCAACCTAACTGTTGAACGGTCCTGTTCTGGCAACGGTGAGAATGCACCTA 2867

QY 121 ATGGACGGGACAACACTTCTTTACCGGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 180
Db 2866 ATGGACGGGACAACACTTCTTTACCGGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 2807

QY 181 TGAGGTGCTTTGCCCATGACCGTCCTTGGTTGTCAGTCACTTGGCACGCTTGCACCG 240
Db 2806 TGAGGTGCTTTGCCCATGACCGTCCTTGGTTGTCAGTCACTTGGCACGCTTGCACCG 2747

QY 241 TGACTCACTGCCACATTGCCCGCGCGTCGCGCGCGCTACAAAAGCCACACACGACG 300
Db 2746 TGACTCACTGCCACATTGCCCGCGCGTCGCGCGCGCTACAAAAGCCACACACGACG 2687

QY 301 CCGGCCACGATAACCCCATCCTAGCATCCCGGTGTCAGCAAGAGATCCATCAAGCGTCG 360
Db 2686 CCGGCCACGATAACCCCATCCTAGCATCCCGGTGTCAGCAAGAGATCCATCAAGCGTCG 2627

QY 361 CGATG 365
Db 2626 CGATG 2622

RESULT 7
AAV23239
ID AAV23239 standard; DNA; 5349 BP.
AC AAV23239;
XX
DT 17-JUL-1998 (first entry)
XX
DE T-DNA of pTTS24.
XX
KW Barstar; barnase inhibitor; fertility restoration;
KW male-sterile line; plasmid pTTS24; T-DNA; ds.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature complement (1..25)
FT /*tag= a
FT /label= RB
FT /note= "right boarder"
FT complement (98..331)
FT /*tag= b
FT /label= 3'-g7
FT /note= "region containing 3' untranslated end of
FT Agrobacterium T-DNA gene 7"
FT CDS 332..883
FT /*tag= c
FT /label= bar
FT /note= "region coding for phosphinothricin acetyl
FT transferase"
FT promoter complement (884..2258)
FT /*tag= d
FT /label= P35S
FT /note= "35S promoter of Cauliflower Mosaic Virus"
FT 2281..3969
FT /*tag= e
FT /label= PE1
FT /note= "promoter of E1 gene of rice (WO9213956)"
FT 3970..4245
FT /*tag= f
FT /product= improved_barstar
FT 4246..4577
FT /*tag= g
```

```
FT /label= 3'_chs
FT /note= "region containing 3' untranslated end of
FT chalcone synthase gene"
FT complement (5325..5349)
FT /*tag= h
FT /note= "T-DNA left border"
PN WO9810081-A2.
XX
XX 12-MAR-1998.
XX
XX 01-SEP-1997; 97WO-EP04739.
XX
XX 03-SEP-1996; 96EP-0202446.
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Michiels F, Williams M;
XX WPI; 1998-193630/17.
XX
XX DNA encoding an improved barstar protein - used to restore fertility
XX in male-sterile plant lines
XX
XX Example 4; Pages 41-43; 54pp; English.
XX
XX The present sequence was used in the preparation of an improved
XX Bacillus amyloliquefaciens barstar, i.e. barnase inhibitor, which
XX can be used to restore fertility to male-sterile lines.
XX The DNA sequence encoding the improved barstar, leads to increased
XX barstar production in tapetum cells, due to improved translation,
XX and possibly protein stability.
XX
XX Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 other;
SQ
Query Match 100.0%; Score 365; DB 19; Length 5349;
Best Local Similarity 100.0%; Pred. No. 6.1e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAGCCAGACCAATGGGGGCAAAATTACTACTATTGGCATACATTAAACCACGTAAAAG 60
Db 3608 TCAGCCAGACCAATGGGGGCAAAATTACTACTATTGGCATACATTAAACCACGTAAAAG 3667

QY 61 TCCTACTACTCAACCTAACTGTTGAACGGTCCTGTTCTGGCCAACGGTGAGAATGCACCTA 120
Db 3668 TCCTACTACTCAACCTAACTGTTGAACGGTCCTGTTCTGGCCAACGGTGAGAATGCACCTA 3727

QY 121 ATGGACGGGACAACACTTCTTTACCGGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 180
Db 3728 ATGGACGGGACAACACTTCTTTACCGGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 3787

QY 181 TGAGGTGCTTTGCCCATGACCGTCCTTGGTTGTCAGTCACTTGGCACGCTTGCACCG 240
Db 3788 TGAGGTGCTTTGCCCATGACCGTCCTTGGTTGTCAGTCACTTGGCACGCTTGCACCG 3847

QY 241 TGACTCACTGCCACATTGCCCGCGCGTCGCGCGCGCTACAAAAGCCACACACGACG 300
Db 3848 TGACTCACTGCCACATTGCCCGCGCGTCGCGCGCGCTACAAAAGCCACACACGACG 3907

QY 301 CCGGCCACGATAACCCCATCCTAGCATCCCGGTGTCAGCAAGAGATCCATCAAGCGTCG 360
Db 3908 CCGGCCACGATAACCCCATCCTAGCATCCCGGTGTCAGCAAGAGATCCATCAAGCGTCG 3967

QY 361 CGATG 365
Db 3968 CGATG 3972

RESULT 8
AAZ91097/c
ID AAZ91097 standard; DNA; 6539 BP.
XX
AC AAZ91097;
```



```
XX 06-JUN-2000 (first entry)
DT
XX E. coli plasmid pTS431 containing mutant barnase gene.
DE
XX Male sterile plant; mutant barnase gene; anther-specific expression;
KW low fidelity PCR; primer; plant breeding; ss.
KW
XX Synthetic.
XX
XX WO200008176-A1.
PN
XX 17-FEB-2000.
PD
XX 03-AUG-1999; 99WO-JP04167.
PF
XX 04-AUG-1998; 98JP-0220060.
PR
XX (NISB ) JAPAN TOBACCO INC.
PA
XX Hamada K, Nakakido F;
PI
XX WPI; 2000-195581/17.
DR
XX Mutate barnase gene for efficient construction of plant transformants,
PT particularly male sterile plants free from any undesirable characters
PT by specifically expressing the gene alone in anther -
XX
PS Example 3; Page 23-27; 30pp; Japanese.
XX
CC The invention relates to the generation of male sterile plants by
CC the introduction of a mutant barnase gene (AAZ91095) for expression
CC specifically in the anther of a plant. This sequence represents the
CC E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains
CC the mutated barnase gene (AAZ91095) under control of the cauliflower
CC mosaic virus 35S promoter. The vector also contains a region of the
CC Agrobacterium T-DNA gene 7. The vector is used for transmitting the
CC barnase gene to plants via an Agrobacterium tumefaciens host cell.
CC The transformed plant is used in plant breeding.
XX
SQ Sequence 6539 BP; 1755 A; 1578 C; 1519 G; 1687 T; 0 other;

Query Match 100.0%; Score 365; DB 21; Length 6539;
Best Local Similarity 100.0%; Pred. NO. 6.7e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 60
Db ||||||
2977 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 2918

QY 61 TCCTACACTCAACCTAACTGTGAACGGTGCTCTGTTCTGCCCAACGGTGAGAAATGCACCTA 120
Db ||||||
2917 TCCTACACTCAACCTAACTGTGAACGGTGCTCTGTTCTGCCCAACGGTGAGAAATGCACCTA 2858

QY 121 ATGGACGGGACACACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 180
Db ||||||
2857 ATGGACGGGACACACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 2798

QY 181 TGAGGTGCTTTTCGCCATGACCGTCTTGGTTGTTGAGTCACTTGGCAGCGCTTGCACCG 240
Db ||||||
2797 TGAGGTGCTTTTCGCCATGACCGTCTTGGTTGTTGAGTCACTTGGCAGCGCTTGCACCG 2738

QY 241 TGAATCACCCTGCCACATTGCCCGCCCGCGTCCGCGGCTACAAAAGCCACACGACGACG 300
Db ||||||
2737 TGAATCACCCTGCCACATTGCCCGCCCGCGTCCGCGGCTACAAAAGCCACACGACGACG 2678

QY 301 CCGGCACGATAACCCATCCTAGCATCCCGGTGTCCACGAAGAGATCCATCAACGCGTCG 360
Db ||||||
2677 CCGGCACGATAACCCATCCTAGCATCCCGGTGTCCACGAAGAGATCCATCAACGCGTCG 2618

QY 361 CGATG 365
Db |||||
2617 CGATG 2613
```

```
RESULT 9
AAT61394/c
ID AAT61394 standard; DNA; 6548 BP.
XX
AC AAT61394;
XX
DT 07-MAY-1997 (first entry)
XX
DE Plasmid pTS172.
XX
KW Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP;
KW niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
KW ribonuclease; RNase; cereal; wheat; Triticum aestivum;
KW plasmid pTS172; ds.
XX
OS Chimeric Agrobacterium sp.;
OS Chimeric Oryza sativa;
OS Chimeric cauliflower mosaic virus.
XX
FH Key Location/Qualifiers
FT 3'UTR complement (2019..2288)
FT /*tag= a
FT /label= 3'nos
FT /note= "3' untranslated region contg. the poly-A
FT signal of Agrobacterium T-DNA nopaline
FT synthase gene"
FT CDS complement (2289..2624)
FT /*tag= b
FT /product= barnase
FT promoter complement (2625..4313)
FT /*tag= c
FT /label= PE1
FT /note= "promoter region of rice E1 gene"
FT promoter complement (4336..5710)
FT /*tag= d
FT /label= p35S
FT /note= "35S promoter region of cauliflower mosaic
FT virus"
FT CDS 5711..6262
FT /*tag= e
FT /label= Bar
FT /note= "phosphinothricin acetyltransferase"
FT 3'UTR 6243..6496
FT /*tag= f
FT /label= 3'g7
FT /note= "3' untranslated region contg. the poly-A
FT signal of gene 7 of Agrobacterium T-DNA"
XX
PN EP757102-A1.
XX
PD 05-FEB-1997.
XX
PF 04-AUG-1995; 95EP-0401844.
XX
PR 04-AUG-1995; 95EP-0401844.
XX
PA (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
PI De Block M;
XX
DR WPI; 1997-1111050/11.
XX
PT Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase
PT inhibitor - reduces the cultured cells response to stress and
PT reduces metabolism
XX
PS Example 2; Page 17-20; 25pp; English.
XX
CC Plasmid pTS172 (AAT61394) contains the barnase coding sequence under
CC control of the rice E1 gene stamen-specific promoter and a
CC phosphinothricin acetyltransferase coding sequence under control of
```

CC the CamV 35S promoter. Plasmid pTS172 and plasmid pTS772 (see also
CC AAT61395) were used to transform wheat Spring variety Pavon calli via
CC particle bombardment. Some calli were treated with the poly-(ADP-
CC ribose) polymerase inhibitor niacinamide before, or before and
CC after, bombardment. Healthy, male sterile plants were regenerated
CC only from bombarded calli that were treated with niacinamide. This
CC was believed to be due to more faithful expression characteristics
CC of the integrated stamen-selective batnase gene in these calli
CC and regenerated shoots. For plants transformed with pTS172,
CC foreign DNA was stably incorporated in the wheat genome in 2-3
CC copies.
XX
SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 100.0%; Score 365; DB 18; Length 6548;
Best Local Similarity 100.0%; Pred. No. 6.7e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAACCCACGTAAAG 60
Db TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAACCCACGTAAAG 2927

QY 61 TCCTACACTCAACCTAACCTGTTGAACGGTCTGTCTGGCCAAACGGTGAGAATGCACCTA 120
Db TCCTACACTCAACCTAACCTGTTGAACGGTCTGTCTGGCCAAACGGTGAGAATGCACCTA 2867

QY 121 ATGGACGGGGACAACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGG 180
Db ATGGACGGGGACAACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGG 2807

QY 181 TGAGGTGCTTTGGCCATGACCGTCTGTTGGTGTGAGTCACTTGGCGACGCTTGCACCG 240
Db TGAGGTGCTTTGGCCATGACCGTCTGTTGGTGTGAGTCACTTGGCGACGCTTGCACCG 2747

QY 241 TGACTCACCTGCCACATTTGCCCGCGCTGCGCGGCTTACAAAGCCACACACGCACG 300
Db TGACTCACCTGCCACATTTGCCCGCGCTGCGCGGCTTACAAAGCCACACACGCACG 2687

QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
Db CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2627

QY 361 CGATG 365
Db 2626 CGATG 2622

RESULT 10
AAZ91096/c
ID AAZ91096 standard; DNA; 6548 BP.
XX
AC AAZ91096;
XX
DT 06-JUN-2000 (first entry)
XX
DE E. coli plasmid pTS172 containing synthetic barnase gene.
XX
KW Male sterile plant; mutant barnase gene; anther-specific expression;
KW low fidelity PCR; primer; plant breeding; ss.
XX
OS Synthetic.
XX
PN WO200008176-A1.
XX
PD 17-FEB-2000.
XX
PF 03-AUG-1999; 99WO-JP04167.
XX
PR 04-AUG-1998; 98JP-0220060.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Hamada K, Nakakido F;

XX WPI; 2000-195581/17.
DR
XX
XX Mutate barnase gene for efficient construction of plant transformants,
XX particularly male sterile plants free from any undesirable characters
XX by specifically expressing the gene alone in anther -
XX
PS Example 3; Page 19-23; 30pp; Japanese.
XX
XX The invention relates to the generation of male sterile plants by
XX the introduction of a mutant barnase gene (AAZ91095) for expression
XX specifically in the anther of a plant. This sequence represents the
XX E. coli/Agrobacterium shuttle vector plasmid pTS172 which contains
XX the synthetic barnase gene (AAZ91094) under control of the cauliflower
XX mosaic virus 35S promoter. The vector also contains a region of the
XX Agrobacterium T-DNA gene 7. The vector is used for transmitting the
XX barnase gene to plants via an Agrobacterium tumefaciens host cell.
XX The transformed plant is used in plant breeding.
SQ Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;

Query Match 100.0%; Score 365; DB 21; Length 6548;
Best Local Similarity 100.0%; Pred. No. 6.7e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAACCCACGTAAAG 60
Db TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCCATACATTAACCCACGTAAAG 2927

QY 61 TCCTACACTCAACCTAACCTGTTGAACGGTCTGTCTGGCCAAACGGTGAGAATGCACCTA 120
Db TCCTACACTCAACCTAACCTGTTGAACGGTCTGTCTGGCCAAACGGTGAGAATGCACCTA 2867

QY 121 ATGGACGGGGACAACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGG 180
Db ATGGACGGGGACAACACTTCTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGG 2807

QY 181 TGAGGTGCTTTGGCCATGACCGTCTGTTGGTGTGAGTCACTTGGCGACGCTTGCACCG 240
Db TGAGGTGCTTTGGCCATGACCGTCTGTTGGTGTGAGTCACTTGGCGACGCTTGCACCG 2747

QY 241 TGACTCACCTGCCACATTTGCCCGCGCTGCGCGGCTTACAAAGCCACACACGCACG 300
Db TGACTCACCTGCCACATTTGCCCGCGCTGCGCGGCTTACAAAGCCACACACGCACG 2687

QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360
Db CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 2627

QY 361 CGATG 365
Db 2626 CGATG 2622

RESULT 11
AAF86441/c
ID AAF86441 standard; DNA; 7492 BP.
XX
AC AAF86441;
XX
DT 25-JUN-2001 (first entry)
XX
DE Plasmid pTS346.
XX
KW Male sterile plant; RNAase inhibitor; plasmid pTS346; ds.
XX
OS Unidentified.
XX
PN WO200124616-A1.
XX
PD 12-APR-2001.
XX
PF 12-SEP-2000; 2000WO-JP06222.

```
XX 30-SEP-1999; 99JP-0279307.
XX (NISB ) JAPAN TOBACCO INC.
XX Hamada K, Nakakido F;
XX WPI; 2001-266212/27.
XX Method for producing male sterile rice and maize by inserting RNase
XX gene and RNase inhibitor genes with promoters into the plant genome -
XX Disclosure; Page 19-23; 29pp; Japanese.
XX The present invention relates to a method for producing male sterile
XX plants. The method comprises inserting a promoter fragment upstream of an
XX RNase gene and a second promoter, upstream of an RNase inhibitor protein
XX gene and inserting it into the plant genome. The method is useful for
XX producing male sterile tobacco, lettuce and rapeseed plants, but
XX preferably rice and maize. The present sequence is a vector used in
XX the method of the present invention.
XX Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;
XX
SQ Query Match 100.0%; Score 365; DB 22; Length 7492;
Best Local Similarity 100.0%; Pred. No. 7.1e-109;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCATACATTAACACGTAAG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
3912 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCATACATTAACACGTAAG 3853

QY 61 TCCTACACTCAACCTAAGTGTGAACGGTCTGTCTTGGCAACGGTGACATGCACCTA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
3852 TCCTACACTCAACCTAAGTGTGAACGGTCTGTCTTGGCAACGGTGACATGCACCTA 3793

QY 121 ATGGACGGGACACACTTCTTCACCGTGTCTACTGCTACATCCTGTAGACGGTGGACGG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
3792 ATGGACGGGACACACTTCTTCACCGTGTCTACTGCTACATCCTGTAGACGGTGGACGG 3733

QY 181 TGAGGTGCTTTGGCCATGACCGTCTTGTGTGTGAGTCACTTGGCCAGCTTGCACCG 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
3732 TGAGGTGCTTTGGCCATGACCGTCTTGTGTGTGAGTCACTTGGCCAGCTTGCACCG 3673

QY 241 TGACTCACCTGCCACATTGCCCGCCGCGCGCGCTACAAAAGCCACACGCGACG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
3672 TGACTCACCTGCCACATTGCCCGCCGCGCGCGCTACAAAAGCCACACGCGACG 3613

QY 301 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCGTCG 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
3612 CCGGCCACGATAACCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCGTCG 3553

QY 361 CGATG 365
Db |||||
3552 CGATG 3548

RESULT 12
AAT39336/C
ID AAT39336 standard; DNA; 6548 BP.
XX
AC AAT39336;
XX
DT 22-JAN-1997 (first entry)
XX
DE Plasmid pTS174 used to obtain male sterile rice.
XX
KW Plasmid pTS174; male sterile; barnase; ribonuclease; transgenic plant;
XX rice; Oryza sativa; ds; cyclic.
OS Synthetic.
XX
FH key, Location/Qualifiers
```

```
FT misc_feature 1..2003
FT /*tag= a
FT /label= Vector
FT /note= "pUC19 derived vector sequences"
FT complement (2019..2283)
FT /*tag= b
FT /label= 3'nos
FT /note= "region containing polyadenylation signal
FT nopaline synthase gene of Agrobacterium
FT T-DNA"
FT complement (2284..2624)
FT /*tag= c
FT /label= Barnase
FT /product= Bacillus amyloliquefaciens barnase
FT complement (2625..4333)
FT /*tag= d
FT /label= PE1
FT /function= promoter of the stamen-specific E1 gene
FT of rice
FT 4336..5710
FT /*tag= e
FT /label= P35S
FT /function= 35S promoter of cauliflower mosaic virus
FT 5711..6262
FT /*tag= f
FT /label= bar
FT /product= phosphinothricin acetyltransferase
FT 6263..6496
FT /*tag= g
FT /label= 3'g7
FT /function= region containing polyadenylation signal
XX
XX WO9626283-A1.
XX
XX 29-AUG-1996.
XX
XX 21-FEB-1996; 96WO-EP00722.
XX
XX 21-FEB-1995; 95EP-0400364.
XX
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Botterman J, Cornelissen M, Michiels F;
XX
XX WPI; 1996-402373/40.
XX
XX Prodn. of male sterile plants by transforming with a chimaeric
XX construct - comprising a male sterility DNA e.g. barnase and a
XX co-regulating gene, e.g. barstar, into the nuclear genome, useful
XX for generating hybrid cultivars
XX
XX Example 1; Page 33-37; 56pp; English.
XX
XX Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control
XX of the stamen-specific PE1 promoter. Embryogenic callus from rice
XX cv. Kochihibiki was transformed with pTS174 alone or with pTS88
XX (see also AAT39337), a plasmid contg. barstar DNA under control of a
XX 35S promoter. With pTS174 alone, 1 male sterile line was recovered
XX from 48 electroporation cuvettes. With both plasmids, 7 normal
XX male sterile lines were recovered from 40 cuvettes. Barnase
XX expression disturbed the function of stamen cells leading to male
XX sterility. Constitutive expression of barstar counteracted any low
XX level expression of barnase in non-stamen tissue.
XX
XX Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;
XX
SQ Query Match 99.6%; Score 363.4; DB 17; Length 6548;
Best Local Similarity 99.7%; Pred. No. 2.2e-108;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCATACATTAACACGTAAG 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
2986 TCAGCCAGACCAATGGGGCAAAATTTACTACTATTGGCATACATTAACACGTAAG 2927
```


QY 61 TCCTACACTCAACCTAACTGTTGACGGTCCCTGTTCTGGCCCAACGGTGAGAAATGCACCTA 120
Db 2926 TCCTACACTCAACCTAACTGTTGACGGTCCCTGTTCTGGCCCAACGGTGAGAAATGCACCTA 2867
QY 121 ATGGACGGGACACACTTCTTTCCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 180
Db 2866 ATGGACGGGACACACTTCTTTCCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 2807
QY 181 TGAGGTGCTTTCCCATGACCGTCCCTGTTGTTGGCAGTCACTTGGCAGCGCTTGCACCG 240
Db 2806 TGAGGTGCTTTCCCATGACCGTCCCTGTTGTTGGCAGTCACTTGGCAGCGCTTGCACCG 2747
QY 241 TGACTCACCTGCGACATGCGCCCGCGCGTCCGCGGCGCTACAAAAGCCACACACGCG 300
Db 2746 TGACTCACCTGCGACATGCGCCCGCGCGTCCGCGGCGCTACAAAAGCCACACACGCG 2687
QY 301 CCGGCCACGATACCCCATCCTAGCATCCCGGTGTCAGCAAGAGATCCATCAAGCCGTCG 360
Db 2686 CCGGCCACGATACCCCATCCTAGCATCCCGGTGTCAGCAAGAGATCCATCAAGCCGTC 2627
QY 361 CGATG 365
Db 2626 CGATG 2622
RESULT 13
AAD03878
ID AAD03878 standard; DNA; 6667 BP.
AC AAD03878;
XX
DT 02-JUL-2001 (first entry)
XX
DE NotI fragment of plasmid pADP73 comprising deacetylase coding sequence.
XX
KW Deacetylase; hybrid seed; wheat; stamen selective promoter; maize; pea;
KW male-sterile cereal crop; chimeric; acetylated toxin; plasmid pADP73;
KW N-acetyl phosphinothricin; N-acetyl ppt; El promoter; NotI fragment;
KW Cauliflower mosaic virus; CaMV; rice; ds.
XX
OS Chimeric - Stenotrophomonas sp.
OS Chimeric - Zea mays.
OS Chimeric - Agrobacterium tumefaciens.
OS Chimeric - Cauliflower mosaic virus.
OS Chimeric - Pisum sativum.
OS Chimeric - Unidentified.
OS Chimeric - Oryza sativa.
XX
FH Key Location/Qualifiers
FT misc_feature 12..35
FT /*tag= a
FT /note= "Left T-DNA border from pTIT37 of A. tumefaciens
(counterclockwise)"
FT 77..130
FT misc_feature
FT /*tag= b
FT /note= "Target sequence for frt/flp excision system"
FT 157..1061
FT /*tag= c
FT /label= Ubiquitin_promoter
FT /note= "Derived from maize"
FT 1062..1142
FT /*tag= d
FT /number= 1
FT /note= "Exon of ubi gene"
FT 1143..2152
FT /*tag= e
FT /number= 1
FT /note= "Intron of ubi gene"
FT 2174..2240
FT 5'UTR
FT /*tag= f
FT /note= "5', untranslated leader sequence from pea
cab22 gene"

FT CDS 2242..2853
FT /*tag= g
FT /product= "Gentamycin acetyltransferase"
FT 2856..3090
FT /*tag= h
FT /note= "Derived from CamV 35S transcript"
FT 3123..3176
FT /*tag= i
FT /note= "Target sequence for frt/flp excision system"
FT 3237..4923
FT /*tag= j
FT /label= pE1_promoter
FT /note= "Derived from rice"
FT 4938..6257
FT /*tag= k
FT /product= "Stenotrophomonas sp. deacetylase (AAE00587)"
FT 6325..6520
FT /*tag= l
FT /note= "Derived from CamV 35S transcript"
FT 6571..6548
FT /*tag= m
FT /note= "Right T-DNA border from pTIT37 of A. tumefaciens
(counterclockwise)"
XX
PN WO200129237-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-EP10281.
XX
PR 15-OCT-1999; 99US-0418617.
XX
PA (AVET) AVENTIS CROPS SCIENCE NV.
PI Quandt J, Bartsch K, Knittel N;
XX
DR WPI: 2001-290923/30.
DR P-PSDB; AAE00587.
XX
PT Producing conditionally male-sterile wheat plants by introducing into
PT genome of wheat cell or tissue foreign DNA having DNA molecule encoding
PT deacetylase under control of stamen selective promoter, regenerating
PT plants
XX
PS Example 2; Page 49-51; 58pp; English.
XX
CC The invention relates to a method for producing male-sterile wheat
CC plants by transforming the wheat plant cell or tissue with chimeric gene
CC comprising DNA molecule encoding deacetylase from Stenotrophomonas sp.
CC deposit number DSM 9734 and a stamen selective promoter like CA55, T72
CC or El. The wheat plant is regenerated from cell or tissue and acetylated
CC toxin (N-acetyl phosphinothricin referred as N-acetyl ppt) is applied to
CC the wheat plant to make it male sterile. The method is useful
CC for producing conditionally male-sterile cereal crops such as barley,
CC rye, oats and most particularly wheat. The conditionally male-sterile
CC plants can be used in wheat breeding to produce composite hybrid wheat
CC seed or pure hybrid wheat seed.
CC The present sequence is a NotI fragment of plasmid pADP73 containing
CC a marker gene cassette and deac (deacetylase) gene expression cassette.
CC The marker gene cassette comprises Ubiquitin promoter from maize
CC containing its first exon and first intron, linked to the 5' untranslated
CC leader sequence of the cab22 gene from pea, operably linked to the
CC gentamycin acetyltransferase (GAT) coding sequence and the 3'
CC untranslated (UTR) sequence from the cauliflower mosaic virus (CaMV) 35S
CC transcript. The whole marker gene cassette is flanked by frt1/frt2
CC sequences as part of the flp/frt excision system. The NotI fragment also
CC contains a deac gene expression cassette comprising the tapetum-specific
CC promoter El from rice operably linked to the deac coding sequence and
CC the 3' UTR from the CaMV 35S transcript. The complete insert is flanked
CC by left and right T-DNA border sequences from Ti-plasmid pTIT37 of
CC Agrobacterium tumefaciens.
XX
SQ Sequence 6667 BP; 1644 A; 1675 C; 1612 G; 1736 T; 0 other;

Query Match 98.7%; Score 360.4; DB 22; Length 6667;
Best Local Similarity 99.7%; Pred. No. 2.2e-107;
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 60
Db 4564 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 4623

QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCTCTGTTCTGGCCAAACGGTGAGAAATGCACCTA 120
Db 4624 TCCTACACTCAACCTAACTGTTGAACGGTCTCTGTTCTGGCCAAACGGTGAGAAATGCACCTA 4683

QY 121 ATGGACGGGACAAACACTTCTTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 180
Db 4684 ATGGACGGGACAAACACTTCTTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 4743

QY 181 TGAGGTGCTTTTCGCGATGACCGTCTCTGTTGTCAGTCACTTGGCGACGCTTGCACCG 240
Db 4744 TGAGGTGCTTTTCGCGATGACCGTCTCTGTTGTCAGTCACTTGGCGACGCTTGCACCG 4803

QY 241 TCACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCTACAAAAGGCACACACGCGACG 300
Db 4804 TCACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCTACAAAAGGCACACACGCGACG 4863

QY 301 CGGGCCACGATACCCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTGC 360
Db 4864 CGGGCCACGATACCCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTGC 4923

QY 361 CG 362
Db 4924 GG 4925

RESULT 14
AAD03888
ID AAD03888 standard; DNA; 1687 BP.
XX
AC AAD03888;
XX
DT 02-JUL-2001 (first entry)
XX
DE E1 promoter from rice.
XX
KW Deacetylase; hybrid seed; wheat; stamen selective promoter; E1 promoter;
KW male-sterile cereal crop; acetylated toxin; N-acetyl phosphinothricin;
KW N-acetyl PPT; rice; ds.
XX
OS Oryza sativa.
XX
PN WO200129237-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-EP10281.
XX
PR 15-OCT-1999; 99US-0418817.
XX
PA (AVET) AVENTIS CROPS SCIENCE NV.
XX
PI Quandt J, Bartsch K, Knittel N;
XX
DR WPI; 2001-290923/30.
XX
PT Producing conditionally male-sterile wheat plants by introducing into
PT genome of wheat cell or tissue foreign DNA having DNA molecule encoding
PT deacetylase under control of stamen selective promoter, regenerating
PT plants -
XX
PS Claim 8; Page 58; 58pp; English.
XX
GC The invention relates to a method for producing male-sterile wheat
GC plants by transforming the wheat plant cell or tissue with chimeric gene

CC comprising DNA molecule encoding deacetylase from Stenotrophomonas sp.
CC deposit number DSM 9734 and a stamen selective promoter like CA55, T72
CC or E1. The wheat plant is regenerated from cell or tissue and acetylated
CC toxin (N-acetyl phosphinothricin referred as N-acetyl PPT) is applied to
CC the wheat plant to make it male sterile. The method is useful
CC for producing conditionally male-sterile cereal crops such as barley,
CC rye, oats and most particularly wheat. The conditionally male-sterile
CC plants can be used in wheat breeding to produce composite hybrid wheat
CC seed or pure hybrid wheat seed.
CC The present sequence is stamen selective promoter E1 promoter from
CC rice.
CC Note: The present sequence is described as a chimeric gene comprising
CC deacetylase coding sequence and E1 promoter sequence throughout the
CC specification. However, the sequence contains only the E1 promoter.
XX
SQ Sequence 1687 BP; 502 A; 381 C; 354 G; 450 T; 0 other;

Query Match 98.6%; Score 360; DB 22; Length 1687;
Best Local Similarity 100.0%; Pred. No. 1.6e-107;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 60
Db 1328 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACCACGTAAAG 1387

QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCTCTGTTCTGGCCAAACGGTGAGAAATGCACCTA 120
Db 1388 TCCTACACTCAACCTAACTGTTGAACGGTCTCTGTTCTGGCCAAACGGTGAGAAATGCACCTA 1447

QY 121 ATGGACGGGACAAACACTTCTTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 180
Db 1448 ATGGACGGGACAAACACTTCTTTTCACCGTGCTACTGCTACATCCTGTAGACGGTGGACGCG 1507

QY 181 TGAGGTGCTTTTCGCGATGACCGTCTCTGTTGTCAGTCACTTGGCGACGCTTGCACCG 240
Db 1508 TGAGGTGCTTTTCGCGATGACCGTCTCTGTTGTCAGTCACTTGGCGACGCTTGCACCG 1567

QY 241 TCACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCTACAAAAGGCACACACGCGACG 300
Db 1568 TCACTCACCTGCCACATTGCCCGCGCGTCCGCGCGCTACAAAAGGCACACACGCGACG 1627

QY 301 CGGGCCACGATACCCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTGC 360
Db 1628 CGGGCCACGATACCCCATCCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTGC 1687

RESULT 15
AAQ10213
ID AAQ10213 standard; DNA; 1831 BP.
XX
AC AAQ10213;
XX
DT 17-DEC-2001 (updated)
DT 27-MAR-1991 (first entry)
XX
DE BamHI G-P-J fragment carrying sequences characteristic of latent
DE pseudorabies virus.
XX
KW PRV; ss.
XX
OS Pseudorabies virus.
XX
PN USN7537855-N.
XX
PD 18-DEC-1990.
XX
PF 13-JUN-1990; 90US-0238940.
XX
PR 13-JUN-1990; 90US-0537855.
XX
PA (USDA) US AGRIC RES SERV.
XX
PI Cheung AK;

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XX
DR      WP1; 1991-021957/03.
XX
PT      Pseudo-rabies virus nucleotide sequences - used for producing
PT      nucleic acid probes, antigens and antibodies for distinguishing
PT      latent from productive infection
XX
PS      Disclosure; Page 22; 27pp; English.
XX
CC      The fragment carries sequences characteristic of the latent
CC      pseudorabies viral genome, and may be used as a probe in diagnosis
CC      of infection.
CC      (Note: Revised entry submitted to correct the patent number format of
CC      US Government-owned NTIS applications to prevent clashes with ongoing US
CC      granted patent numbers. For further information please visit the Derwent
CC      web site at www.derwent.com/dwpi/updates/ntis\_us.html.)
XX
SQ      Sequence 1831 BP; 305 A; 643 C; 639 G; 244 T; 0 other;

      Query Match          9.6%; Score 35.2; DB 12; Length 1831;
      Best Local Similarity 54.7%; Pred. NO. 0.46;
      Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY      194 CCATGACCGTCCTTGGTTGTTGCAGTCACTTGCGCACGCTTGACACCGTGACTCACCTGCC 253
      || | ||| || | || | | ||| || | || | ||| ||
Db      1537 CCGTCGCGCGCCGCGGTGCGTGCGAGCGCCCGGGAACCCCGGCCCAACACACACCGGCA 1596

QY      254 ACATTGCCCGCGCGCGTCGCGCGGCGCTACAAAGCGCACACACGCGCGCGGCCACGATAA 313
      || | ||| || | ||| || | | ||| ||| ||| ||| ||
Db      1597 CCACCACCGGCATCATCGTCCCGCCCTCTCCACATACACGCTCGCACTCGGCGCCACACGCT 1656

QY      314 CCCATCCT 321
      ||| ||||
Db      1657 CCCGTCCT 1664

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Search completed: December 2, 2002, 01:40:50
Job time : 101.721 secs

